Amendments to the Specification:

Please delete the paragraph on p. 1, lines 5-16, and replace it with the following paragraph:

The present application ~~claims benefit under 35 U.S.C. § 120 as a continuation-in-part of U.S. Patent Application Serial No. 08/430,938, filed April 27, 1995, which is a continuation-in-part of U.S. Patent Application Serial Nos. 08/234,143, 08/112,848, 08/031,801, 07/919,297, 07/610,515, and 07/466,008 (filed April 28, 1994, August 27, 1993, March 15, 1993, July 24, 1992, November 8, 1990 and January 12, 1990, respectively)~~ is a continuation of United States application 09/614,092, which is a continuation of United States application 08/724,752, filed October 2, 1996, now United States Patent No. 6,150,584, which is a continuation-in-part of United States application 08/430,938, filed April 27, 1995, now abandoned, which is a continuation-in-part of United States application 08/234,145, filed April 28, 1994, now abandoned, which is a continuation-in-part of United States application 08/112,848, filed August 27, 1993, now abandoned, which is a continuation of United States application 08/031,801, filed March 15, 1993, which is a continuation-in-part of United States application 07/919,297, filed July 24, 1992, now abandoned, which is a continuation-in-part of United States application 07/610,515, filed November 8, 1990, now abandoned, which is a continuation-in-part of United States application 07/466,008, filed January 12, 1990, now abandoned. The present application also claims benefit under 35 U.S.C. § 119 to PCT/US96/05928, filed April 29, 1996. The

disclosures of each of the aforementioned applications are hereby incorporated by reference in their entirety.

Please delete the two paragraphs on p. 5, lines 14-19, and replace them with the following two paragraphs:

Figure 12 DNA sequence (SEQ ID NO:2) of the heavy chain of anti-tetanus toxin monoclonal antibody D5.1.4 (a subclone of D5.1). Mutations ~~form~~ from germline are boxed. The DNA sequences of germline VH6, JH4, D(N1) and hMu are SEQ ID NOs:1, 3, 4 and 5, respectively.

Figure 13 DNA sequence (SEQ ID NO:7) of the kappa light chain of anti-tetanus toxin monoclonal antibody D5.1.4. Mutations ~~form~~ from germline are boxed. The DNA sequences of germline B3, JK3 and CK are SEQ ID NOs:6, 8 and 9, respectively.

Please delete the paragraph on p. 5, lines 26-28, and replace it with the following paragraph:

Figure 16 (A-H) DNA sequences of the heavy chain (SEQ ID NO:10) and kappa light chain (SEQ ID NO:11) of the anti-IL-8 antibodies D1.1 (16A-B), the heavy chain (SEQ ID NO:12) and the light chain (SEQ ID NO:13) of K2.2 (16C-D), the heavy chain (SEQ ID NO:14) and the light chain (SEQ ID NO:15) of K4.2 (16E-F), and the heavy chain (SEQ ID NO:16) and the light chain (SEQ ID NO:17) of K4.3 (16G-H).

Please delete the two paragraphs on p. 29, lines 21-31, and replace them with the following two paragraphs:

The cell line was known to provide human κ light chains; for PCR amplification of light chain encoding cDNA, the primers used were HKP1 (5' - CTCTGTGACACTCTCCTGGGAGTT - 3') (SEQ ID NO:18) for priming from the constant region terminus and two oligos, used in equal amounts to prime from the variable segments; B3 (5' - GAAACGACACTCACGCAGTCTCCAGC - 3') (SEQ ID NO:19).

For amplification of the heavy chain of the antibody derived from D5.1 (which contains the human μ constant region), MG-24VI was used to prime from the variable and μP1 (5' - TTTTCTTTGTTGCCGTTGGGGTGC - 3') (SEQ ID NO:20) was used to prime from the constant region terminus.

Please delete the paragraph on page 41, lines 3-17, and replace it with the following paragraph:

All sequences were derived by direct sequencing of PCR fragments generated ~~form~~ from RT-PCR reactions of RNA prepared from hybridomas D1.1, K2.2, K4.2 and K4.3, using human V_H and human $V_κ$ family specific primers (Marks et al., 1991~~,~~ Euro J. Immunol 21~~:~~:985-991) and a primer specific for either the human gamma 2 constant region (MG-40d; 5' GCTGAGGGAGTAGAGTCCTGAGGACTGT - 3') (SEQ ID NO:21) or human kappa constant region (HKP2; Green et ~~al~~ al., 1994~~,~~ Nature Genetics 7:13-21)). In Figure 16 A-H, both strands of the four clones were sequenced and analyzed to generate the complete sequence. All sequences were analyzed by alignments to the "V BASE sequence directory", Tomlinson *et al.*, MRC Centre for Protein Engineering, Cambridge, UK. The variable and joining regions are

indicated by brackets []. Nucleotides containing an "N" indicate uncertainty in the generated sequence.

Please insert the Sequence Listing (pages 1-8) submitted herewith at the end of the application after the abstract.